

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Flavonoid Biosynthetic Enzymes

<130> BB1324

<140>

<141>

<150> 60/113,190

<151> 1998-12-21

<160> 6

<170> Microsoft Office 97

<210> 1

<211> 1859

<212> DNA

<213> Glycine max

<400> 1

```

gaaaacactg acagacagca tagtctctgg tgcaagaatc aattgagcaa gcatgggaat 60
gttggttggtg gtggttctcat acgctgtcct ttctcctggtt ctattcctcg gcgtgaagtt 120
tgttttccaa agcagaaaat tgagaaacat accaccaggt cctcctcctc ttcccataat 180
aggaaacctt aacctcctcg aacagccaat ccaccgtttc ttccaacgca tgtcgaaaca 240
gtacggcaac gtggtttccc tctggttcgg ttacgctctg gccgttgtca tctcctctcc 300
aacagcatat caagaatgct tcaccaaaca cgacgttgcc ttggccaacc ggctaccttc 360
tctctcggga aaatacatct tctacaacaa caccaccgta ggctcctgct cccacggcga 420
gcaactggcg aacctccgcc gcatcaccgc cctggacgtc ctctccacgc agcgcgtcca 480
ctccttctcc ggaatccgga gcgacgagac gaagcgtctg atgcagaggt tgggtgctggc 540
caagaactcg aacgaggaag agtttgccgc agtggagatt agttcgatgt tcaacgactt 600
aacttacaac aacataatga ggatgatata ggggaagagg ttttacggag aggagagtga 660
gatgaagaac gttgaggaag cgagggaggt cagagagact gtgacagaaa tgttggaact 720
catgggcttg gctaacaagg gagatcactt gcctttcctc aggtgggttcg attttcagaa 780
tgtggagaag cgcttaaaga gtatcagtaa gaggtacgat tccatcttga ataagatcct 840
tcatgagaac cgtgccagca atgaccgcca gaattccatg atcgatcatc tcctcaaact 900
gcaagagacc cagcctcagt actacactga ccaaatacat aaaggccttg ctctggccat 960
gctttttggt ggaactgact catcaactgg gactttagag tggtcattat ctaatttatt 1020
gaatcaccca gaggtgttga agaaggcaag agatgaattg gacactcaag tgggacaaga 1080
ccgcttggtt aatgagtcag accttccaaa acttccatat cttaggaaga tcacccctga 1140
gacacttagg ttgtaccccc cggccccaat tctaatacct catgtgtctt cagaagatat 1200
tacaattgaa ggattcaata tcccacgaga cacaattgtg atcattaatg gttggggcat 1260
gcagagagat cctcagttgt ggaatgatgc cacatgcttt aaacctgaga ggtttgatgt 1320
ggaaggagag gagaaaaagt tggtagcatt tggcatggga agaagggtct gccacggaga 1380
acccatggct atgcaaagtg tcagctttac tttgggattg ttgattcaat gttttgactg 1440
gaaacgagta agtgaggaaa agcttgatat gacagagaac aattggatca ccttgtcaag 1500
gttaattcca ttggaggcca tgtgcaaggc tcgcccactt gccactaaaa ttggaattta 1560
attattaata gtatttttat ttggtaaact tgggtgattc agaactctaat acttataatt 1620
ttagtgtgta agagtgggtga tcatatatac atttcaaaat taataatctt tgtccaaaaa 1680
tcattccatg acaactatat gtcaattgac atctagagag aaatatagat ataagaatat 1740
ttatatatta ttactcttct ttatcttatg tgtcaaggcc cattgtagaa ttgggtgagc 1800
attaacatat atcaatattg tataccgccc agttttctca aataaatttc ttactttc 1859

```

<210> 2

<211> 499

<212> PRT

<213> Glycine max

<400> 2

Leu Leu Val Val Val Ser Tyr Ala Val Leu Phe Leu Val Leu Phe Leu
 1 5 10 15
 Gly Val Lys Phe Val Phe Gln Ser Arg Lys Leu Arg Asn Ile Pro Pro
 20 25 30
 Gly Pro Pro Pro Leu Pro Ile Ile Gly Asn Leu Asn Leu Leu Glu Gln
 35 40 45
 Pro Ile His Arg Phe Phe Gln Arg Met Ser Lys Gln Tyr Gly Asn Val
 50 55 60
 Val Ser Leu Trp Phe Gly Ser Arg Leu Ala Val Val Ile Ser Ser Pro
 65 70 75 80
 Thr Ala Tyr Gln Glu Cys Phe Thr Lys His Asp Val Ala Leu Ala Asn
 85 90 95
 Arg Leu Pro Ser Leu Ser Gly Lys Tyr Ile Phe Tyr Asn Asn Thr Thr
 100 105 110
 Val Gly Ser Cys Ser His Gly Glu His Trp Arg Asn Leu Arg Arg Ile
 115 120 125
 Thr Ala Leu Asp Val Leu Ser Thr Gln Arg Val His Ser Phe Ser Gly
 130 135 140
 Ile Arg Ser Asp Glu Thr Lys Arg Leu Met Gln Arg Leu Val Leu Ala
 145 150 155 160
 Lys Asn Ser Asn Glu Glu Glu Phe Ala Arg Val Glu Ile Ser Ser Met
 165 170 175
 Phe Asn Asp Leu Thr Tyr Asn Asn Ile Met Arg Met Ile Ser Gly Lys
 180 185 190
 Arg Phe Tyr Gly Glu Glu Ser Glu Met Lys Asn Val Glu Glu Ala Arg
 195 200 205
 Glu Phe Arg Glu Thr Val Thr Glu Met Leu Glu Leu Met Gly Leu Ala
 210 215 220
 Asn Lys Gly Asp His Leu Pro Phe Leu Arg Trp Phe Asp Phe Gln Asn
 225 230 235 240
 Val Glu Lys Arg Leu Lys Ser Ile Ser Lys Arg Tyr Asp Ser Ile Leu
 245 250 255
 Asn Lys Ile Leu His Glu Asn Arg Ala Ser Asn Asp Arg Gln Asn Ser
 260 265 270
 Met Ile Asp His Leu Leu Lys Leu Gln Glu Thr Gln Pro Gln Tyr Tyr
 275 280 285
 Thr Asp Gln Ile Ile Lys Gly Leu Ala Leu Ala Met Leu Phe Gly Gly
 290 295 300

Thr Asp Ser Ser Thr Gly Thr Leu Glu Trp Ser Leu Ser Asn Leu Leu
 305 310 315 320
 Asn His Pro Glu Val Leu Lys Lys Ala Arg Asp Glu Leu Asp Thr Gln
 325 330 335
 Val Gly Gln Asp Arg Leu Leu Asn Glu Ser Asp Leu Pro Lys Leu Pro
 340 345 350
 Tyr Leu Arg Lys Ile Ile Leu Glu Thr Leu Arg Leu Tyr Pro Pro Ala
 355 360 365
 Pro Ile Leu Ile Pro His Val Ser Ser Glu Asp Ile Thr Ile Glu Gly
 370 375 380
 Phe Asn Ile Pro Arg Asp Thr Ile Val Ile Ile Asn Gly Trp Gly Met
 385 390 395 400
 Gln Arg Asp Pro Gln Leu Trp Asn Asp Ala Thr Cys Phe Lys Pro Glu
 405 410 415
 Arg Phe Asp Val Glu Gly Glu Glu Lys Lys Leu Val Ala Phe Gly Met
 420 425 430
 Gly Arg Arg Ala Cys Pro Gly Glu Pro Met Ala Met Gln Ser Val Ser
 435 440 445
 Phe Thr Leu Gly Leu Leu Ile Gln Cys Phe Asp Trp Lys Arg Val Ser
 450 455 460
 Glu Glu Lys Leu Asp Met Thr Glu Asn Asn Trp Ile Thr Leu Ser Arg
 465 470 475 480
 Leu Ile Pro Leu Glu Ala Met Cys Lys Ala Arg Pro Leu Ala Thr Lys
 485 490 495

Ile Gly Ile

<210> 3
 <211> 1698
 <212> DNA
 <213> Glycine max

<400> 3
 cagtaataaac aatgtctcct ttcttatctt actctcttct ttccctcgtg ttcttcttca 60
 ctctcaagta ccttttccaa agaagcagaa aagtacgaaa cctgccacct ggtccgactc 120
 ctcttcctat aatcggaac cttaacctcg ttgaacaacc tatacacctg ttcttccacc 180
 gcatgtccca aaaatatgga aacatcatat ccttttggtt tgggtcacgt cttgttgttg 240
 ttgtttcatc acccacagcg taccaagaat gtttcaccaa acatgatgtt accttgcca 300
 acagggtacg ctccctctcg ggaaaataca tattctacga caacaccacc gtagggctct 360
 gctcccacgg cgagcactgg cgcaacctcc gccgcataac ctctctcgac gttctatcga 420
 cgcagcgcgt ccactccttc tccggaatcc ggagcgacga gacgaagagg ttgatacaca 480
 ggctggccag ggactccggg aaagattttg cgcgcgtgga gatgacctcc aagtttgctg 540
 acttgacgta caacaacatc atgaggatga ttccggggaa gcggttttac ggagaagaga 600
 gtgaacttaa caacgttgag gaagcgaagg agttcagaga cactgtgaat gagatgctgc 660
 aactcatggg gttggctaac aaggagatc acttaccttt cctaagggtg ttcgattttc 720
 agaacgtgga gaagaggttg aagaatatca gtaagaggta tgataccatc ttgaataaga 780
 tccttgatga gaaccgtaac aacaaggacc gcgagaattc catgattggt catctcctca 840
 aactgcaaga gacacagcct gactattata ccgaccaaact catcaaaggc cttgctttgg 900

```

ctatgctctt tgggtggaaca gactcgtcaa ctggaacttt agagtgggca ttatctaatt 960
tagtgaatga cccagagggtg ctgcagaagg caagagatga gttggacgct caagtaggac 1020
cagatcggct gttaaatgag tcagaccttc caaaacttcc ttatctcagg aagatagttc 1080
ttgaaacact taggttgtag cctccggctc caattctaata accacacgtg gcttcagaag 1140
acatcaatat cgaaggattc aatgttccac gagacacaat tgtgattatt aatgggtggg 1200
ccatgcaaag agatcctaag atatggaaag atgcgacaag ctttaaacct gagaggtttg 1260
atgaagaagg agaggagaag aaattggtag catttggtat gggaagaagg gcttgcccag 1320
gagaacccat ggctatgcaa agtggttagct atactttggg attaatagatt caatgttttg 1380
actggaaacg agtaagttag aagaagcttg atatgacaga gaataattgg atcaccttgt 1440
caaggttaat tccattggag gctatgtgta aagcccgcgc actcgccagc aaagttgaaa 1500
gttattaaca atattttatt tggatatatt gggtagaggat ctaataactca taatttcggg 1560
gtgtaagtct atgcatgtta aaattaataa tatttgtcgt atgtccacaa ggccaaatgt 1620
agtactgggt gtggatttgc atatacaata tcaatattgt ataaatccca gtttccttga 1680
ataaatttct ttactttc 1698

```

<210> 4
 <211> 494
 <212> PRT
 <213> Glycine max

<400> 4
 Leu Ser Tyr Ser Leu Leu Ser Leu Val Phe Phe Phe Thr Leu Lys Tyr
 1 5 10 15
 Leu Phe Gln Arg Ser Arg Lys Val Arg Asn Leu Pro Pro Gly Pro Thr
 20 25 30
 Pro Leu Pro Ile Ile Gly Asn Leu Asn Leu Val Glu Gln Pro Ile His
 35 40 45
 Arg Phe Phe His Arg Met Ser Gln Lys Tyr Gly Asn Ile Ile Ser Leu
 50 55 60
 Trp Phe Gly Ser Arg Leu Val Val Val Val Ser Ser Pro Thr Ala Tyr
 65 70 75 80
 Gln Glu Cys Phe Thr Lys His Asp Val Thr Leu Ala Asn Arg Val Arg
 85 90 95
 Ser Leu Ser Gly Lys Tyr Ile Phe Tyr Asp Asn Thr Thr Val Gly Ser
 100 105 110
 Cys Ser His Gly Glu His Trp Arg Asn Leu Arg Arg Ile Thr Ser Leu
 115 120 125
 Asp Val Leu Ser Thr Gln Arg Val His Ser Phe Ser Gly Ile Arg Ser
 130 135 140
 Asp Glu Thr Lys Arg Leu Ile His Arg Leu Ala Arg Asp Ser Gly Lys
 145 150 155 160
 Asp Phe Ala Arg Val Glu Met Thr Ser Lys Phe Ala Asp Leu Thr Tyr
 165 170 175
 Asn Asn Ile Met Arg Met Ile Ser Gly Lys Arg Phe Tyr Gly Glu Glu
 180 185 190
 Ser Glu Leu Asn Asn Val Glu Glu Ala Lys Glu Phe Arg Asp Thr Val
 195 200 205

Asn Glu Met Leu Gln Leu Met Gly Leu Ala Asn Lys Gly Asp His Leu
 210 215 220
 Pro Phe Leu Arg Trp Phe Asp Phe Gln Asn Val Glu Lys Arg Leu Lys
 225 230 235 240
 Asn Ile Ser Lys Arg Tyr Asp Thr Ile Leu Asn Lys Ile Leu Asp Glu
 245 250 255
 Asn Arg Asn Asn Lys Asp Arg Glu Asn Ser Met Ile Gly His Leu Leu
 260 265 270
 Lys Leu Gln Glu Thr Gln Pro Asp Tyr Tyr Thr Asp Gln Ile Ile Lys
 275 280 285
 Gly Leu Ala Leu Ala Met Leu Phe Gly Gly Thr Asp Ser Ser Thr Gly
 290 295 300
 Thr Leu Glu Trp Ala Leu Ser Asn Leu Val Asn Asp Pro Glu Val Leu
 305 310 315 320
 Gln Lys Ala Arg Asp Glu Leu Asp Ala Gln Val Gly Pro Asp Arg Leu
 325 330 335
 Leu Asn Glu Ser Asp Leu Pro Lys Leu Pro Tyr Leu Arg Lys Ile Val
 340 345 350
 Leu Glu Thr Leu Arg Leu Tyr Pro Pro Ala Pro Ile Leu Ile Pro His
 355 360 365
 Val Ala Ser Glu Asp Ile Asn Ile Glu Gly Phe Asn Val Pro Arg Asp
 370 375 380
 Thr Ile Val Ile Ile Asn Gly Trp Ala Met Gln Arg Asp Pro Lys Ile
 385 390 395 400
 Trp Lys Asp Ala Thr Ser Phe Lys Pro Glu Arg Phe Asp Glu Glu Gly
 405 410 415
 Glu Glu Lys Lys Leu Val Ala Phe Gly Met Gly Arg Arg Ala Cys Pro
 420 425 430
 Gly Glu Pro Met Ala Met Gln Ser Val Ser Tyr Thr Leu Gly Leu Met
 435 440 445
 Ile Gln Cys Phe Asp Trp Lys Arg Val Ser Glu Lys Lys Leu Asp Met
 450 455 460
 Thr Glu Asn Asn Trp Ile Thr Leu Ser Arg Leu Ile Pro Leu Glu Ala
 465 470 475 480
 Met Cys Lys Ala Arg Pro Leu Ala Ser Lys Val Glu Ser Tyr
 485 490

<210> 5
 <211> 843
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (476)

<220>
 <221> unsure
 <222> (657)

<220>
 <221> unsure
 <222> (703)

<220>
 <221> unsure
 <222> (712)

<220>
 <221> unsure
 <222> (789)

<220>
 <221> unsure
 <222> (843)

<400> 5
 ttcactctca agcttcaagc atgactcctt tttacttcct cctatttgcc ttcactcctt 60
 tctcttccat aaacttcttg atccaaacaa gaagggtcaa aaaccttctt ccggggaccat 120
 tttctttccc tataatcgga aacctccacc aactcaagca acccctccac cgcacgttcc 180
 atgccttatc acaaaaatat ggccctattt tctccctctg gttcgggtcc cgttttgtcg 240
 tcgtcgtttc gtcgccgctc gcggtgcaag aatgcttcac caagaacgac atcgtcttgg 300
 ccaaccgccc tcaacttctc accggcaagt atatagggtta caacaacacc accgtcgcgcg 360
 tttccccta cggcgaccac tggcgcaacc tccgcgcgat catggcgctc gaggttctct 420
 ccaccacccg gataaactcc ttcttggaat atcggagggg acgaagatca tgaggntcgt 480
 gcaaaaagctt gctcgggact cgcgcaatgg gttcaccaaa gtagaactta aatccagggt 540
 ttcggagatg acatttaaca ctataatgag gatggtgtca ggggaagagg actatggtga 600
 agactgtgat gtgagtgatg tacaggaagc aagcaattta gagagatcat taaagantgg 660
 tgacgttagg aggggctaataaacctgggga ctcttggttt gcntgggtgg tntttgatgg 720
 ttggaaagag cttaaagagga tagtagagaa cgatcggtta caggaccatt gtagcatcta 780
 tggaacacnt gcatacatga taatatctct gccacacaac acaccgatat aacgttaatc 840
 atn 843

<210> 6
 <211> 141
 <212> PRT
 <213> Glycine max

<400> 6
 Phe Leu Leu Phe Ala Phe Ile Leu Phe Leu Ser Ile Asn Phe Leu Ile
 1 5 10 15
 Gln Thr Arg Arg Phe Lys Asn Leu Pro Pro Gly Pro Phe Ser Phe Pro
 20 25 30
 Ile Ile Gly Asn Leu His Gln Leu Lys Gln Pro Leu His Arg Thr Phe
 35 40 45
 His Ala Leu Ser Gln Lys Tyr Gly Pro Ile Phe Ser Leu Trp Phe Gly
 50 55 60

Ser Arg Phe Val Val Val Val Ser Ser Pro Leu Ala Val Gln Glu Cys
65 70 75 80

Phe Thr Lys Asn Asp Ile Val Leu Ala Asn Arg Pro His Phe Leu Thr
85 90 95

Gly Lys Tyr Ile Gly Tyr Asn Asn Thr Thr Val Ala Val Ser Pro Tyr
100 105 110

Gly Asp His Trp Arg Asn Leu Arg Arg Ile Met Ala Leu Glu Val Leu
115 120 125

Ser Thr His Arg Ile Asn Ser Phe Leu Glu Asn Arg Arg
130 135 140